

09471572Results

SEQ ID NO: 1

RESULT 2

S30359

GTP-binding regulatory protein G alpha chain, phospholipase C-activating - turkey

N;Alternate names: phospholipase C-activating G protein

C;Species: Meleagris gallopavo (common turkey)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 02-Feb-2001

C;Accession: S30359; S30360

R;Maurice, D.H.; Waldo, G.L.; Morris, A.J.; Nicholas, R.A.; Harden, T.K.

Biochem. J. 290, 765-770, 1993

A;Title: Identification of Galpha(11) as the phospholipase C-activating G-protein of turkey erythrocytes.

A;Reference number: S30359; MUID:93207527

A;Accession: S30359

A;Molecule type: mRNA

A;Residues: 1-359 <MAU>

A;Cross-references: GB:X73072; NID:g312254; PIDN:CAA51530.1; PID:g312255

A;Experimental source: blood

A;Accession: S30360

A;Molecule type: protein

A;Residues: 78-92;121-132;158-180;253-256;307-312;339-345;355-359 <MAW>

A;Experimental source: erythrocytes

C;Superfamily: GTP-binding regulatory protein Gs alpha chain

C;Keywords: GTP binding; nucleotide binding; P-loop

F;46-53/Region: nucleotide-binding motif A (P-loop)

F;156-158/Region: GTP-binding SAK/L motif

F;274-277/Region: GTP-binding NKXD motif

F;52/Binding site: GTP (Lys) #status predicted

F;183/Modified site: ADP-ribosylarginine (Arg) (by cholera toxin) #status predicted

Query Match 82.0%; Score 1507; DB 2; Length 359;

Best Local Similarity 82.2%; Pred. No. 4.6e-98;

Matches 291; Conservative 25; Mismatches 36; Indels 2; Gaps 1;

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Qy      1 MACCLSEEAREQKRINQEIEKQLQDRKRNARRELKLLLLGTGESGKSTFIKQMRIIHGQG 60
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Db      7 MACCLSDEVKESKRINAEIEKQLRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSG 66

Qy     61 YSEEDKRAHIRLVYQNVFMAIQSMIRAMDTLDIKFGNESEELQEKAADVREVDVESVTSF 120
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Db     67 YSEEDKKGFTKLVYQNIPTAMQSMIRAMETLKILY--KYEQNKANAVLIREVDVEKVMTF 124

Qy    121 EEPYVSYIKELWEDSGIQECYDRRREYQLTDSAKYYLSDLRRLAVPDYLPTEQDILRVRV 180
      |:||| || || | |||||:|||||:|||||:|:| |||||:|:| |||||:|:|
Db    125 EQPYVSAIKTLWNDPGIQECYDRRREYQLSDSAKYYLSVDVRIATPGYLPQDVLVRV 184

Qy    181 PTTGIIIEYFPDLEQIIFRMVDVGGQSRERRKWIHCFENVTSIMFLVALSEYDQVLVECDN 240
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Db    185 PTTGIIIEYFPDLENIIFRMVDVGGQSRERRKWIHCFENVTSIMFLVALSEYDQVLVESDN 244

Qy    241 ENRMEESKALFRTIITYPWFNTSSVILFLNKKDLLEEKILYSHLADYFPEYDGPDPDPIA 300
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Db    245 ENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLEDKILYSHLVDFPEFDGPQDAQA 304

Qy    301 AREFILKMFVDLNPADAKIIYSHFTCATDTENIRFVFAVKDTILQNNLKYIGL 354
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Db    305 AREFILKMFVDLNPDSKIIYSHFTCATDTENIRFVFAVKDTILQLNLKEYNL 358
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RESULT 1

Q17386

ID Q17386 PRELIMINARY; PRT; 355 AA.

AC Q17386; O02546;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE EGL-30 (HETEROTRIMERIC G PROTEIN ALPHA SUBUNIT).
 GN EGL-30 OR M01D7.7.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=N2;
 RX MEDLINE=96221161; PubMed=8630258;
 RA Brundage L., Avery L., Katz A., Kim U.J., Mendel J.E., Sternberg P.W.,
 RA Simon M.I.;
 RT "Mutations in a C. elegans Galpha gene disrupt movement, egg laying,
 RT and viability."
 RL Neuron 16:999-1009(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
 RA Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans."
 RL Nature 368:32-38(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Gattung S., Goela D., Wilson R.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Waterston R.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=N2;
 RA Cuppen E., Jansen G., Plasterk R.H.A.;
 RT "Interaction analysis of the complete G-alpha subfamily of
 RT heterotrimeric G proteins from Caenorhabditis elegans."
 RL Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; U56864; AAB04059.1; -.
 DR EMBL; AF003739; AAB58071.1; -.
 DR EMBL; AY008139; AAG32092.1; -.
 DR HSSP; P10824; 1BOF.
 DR InterPro; IPR001019; Gprotein_alpha.
 DR Pfam; PF00503; G-alpha; 1.
 DR PRINTS; PR00318; GPROTEINA.
 DR SMART; SM00275; G-alpha; 1.
 SQ SEQUENCE 355 AA; 41865 MW; FEA38B01C2E1355C CRC64;

Query Match 98.2%; Score 1804; DB 5; Length 355;
 Best Local Similarity 98.9%; Pred. No. 2.4e-116;
 Matches 350; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MACCLSEEAREQKRINQIEKQLQDRKNARRELKLLLLGTGESGKSTFIKQMRIIHGQG 60
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 Db 1 MACCLSEEAREQKRINQIEKQLQDRKNARRELKLLLLGTGESGKSTFIKQMRIIHGQG 60
 Qy 61 YSEEDKRAHIRLVYQNVFMAIQSMIRAMDTLDIKFGNESEELQEKAADVREVDVFESVTSF 120

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Db      61 YSEEDKRAHIRLVYQNVFMAIQSMIRAMDTLDIKFGNESEELQEKAADVREVDVFESVTSF 120
Qy     121 EEPYVSYIKELWEDSGIQECYDRRREYQLTDSAKYYLSDLRRLAVPDYLPTEQDILRVRV 180
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Qy     181 PTTGIIEYPFDLEQIIFRMVDVGGQSRERRKWIHCFENVTSIMFLVALSEYDQVLVECDN 240
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Qy     241 ENRMEESKALFRTIITYPWFTNSSVILFLNKKDLLEEKILYSHLADYFPEYDGPPRDPIA 300
Db     241 ENRMEESKALFRTIITYPWFTNSSVILFLNKKDLLEEKILYSHLADYFPEYDGPPRDPIA 300
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Db     301 AREFILKMFVDLNPADAKIIYSHFTCATDTENIRFVFAAVKDTILQHNLKEYNL 354

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SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1501	81.7	1276	20	AAY49127	phCaR/hmGluR2*Gqi5
2	1501	81.7	1323	20	AAY49133	GABA-BR1a*Gqo5 fus
3	1501	81.7	1394	20	AAY49129	pmGluR2/CaR*Galpha
4	1501	81.7	1397	20	AAY49134	pmGluR2/CaR*Galpha
5	1501	81.7	1418	20	AAY49131	mGluR8/CaR*Galphaq
6	1497	81.4	359	22	AAB99071	Human G-protein al
7	1497	81.4	359	22	AAB99073	Human G-protein al
8	1495	81.3	353	22	AAB99072	Human G-protein al
9	1494	81.3	1303	20	AAY49132	GABA-BR2*Gqo5 fusi
10	1493	81.2	359	20	AAY49125	Chimeric Gqi5 prot
11	1486	80.8	359	20	AAY52705	Human G-alpha-11 p
12	1486	80.8	359	20	AAY29789	Human G-alpha-11 p
13	1388	75.5	355	21	AAB15026	Mouse TC-Galpha14
14	1385	75.4	355	22	AAB99076	Human G-protein al
15	1029	56.0	374	22	AAB84005	Amino acid sequenc
16	1029	56.0	374	22	AAB84007	Amino acid sequenc
17	1028	55.9	374	22	AAB83997	Amino acid sequenc
18	1028	55.9	374	22	AAB83999	Amino acid sequenc
19	1028	55.9	374	22	AAB84001	Amino acid sequenc
20	1028	55.9	374	22	AAB84006	Amino acid sequenc
21	1028	55.9	374	22	AAB84008	Amino acid sequenc
22	1028	55.9	374	22	AAB84010	Amino acid sequenc
23	1027	55.9	374	22	AAB83978	Amino acid sequenc
24	1027	55.9	374	22	AAB83998	Amino acid sequenc
25	1027	55.9	374	22	AAB84000	Amino acid sequenc
26	1027	55.9	374	22	AAB84009	Amino acid sequenc
27	1024	55.7	374	22	AAB84002	Amino acid sequenc
28	1024	55.7	374	22	AAB84004	Amino acid sequenc
29	1023	55.7	374	22	AAB83996	Amino acid sequenc
30	1023	55.7	374	22	AAB84003	Amino acid sequenc
31	1020	55.5	374	22	AAB83990	Amino acid sequenc
32	1020	55.5	374	22	AAB83992	Amino acid sequenc
33	1019	55.4	374	22	AAB83982	Amino acid sequenc
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35	1019	55.4	374	22	AAB83986	Amino acid sequenc
36	1019	55.4	374	22	AAB83991	Amino acid sequenc
37	1019	55.4	374	22	AAB83993	Amino acid sequenc
38	1019	55.4	374	22	AAB83995	Amino acid sequenc
39	1018	55.4	374	22	AAB83977	Amino acid sequenc
40	1018	55.4	374	22	AAB83983	Amino acid sequenc
41	1018	55.4	374	22	AAB83985	Amino acid sequenc
42	1018	55.4	374	22	AAB83994	Amino acid sequenc
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44	1015	55.2	374	22	AAB83989	Amino acid sequenc
45	1014	55.2	374	22	AAB83981	Amino acid sequenc

SUMMARIES

Result No.	Query		Length	DB	ID	Description
	Score	Match				
1	1804	98.2	355	2	T15288	hypothetical prote
2	1507	82.0	359	2	S30359	GTP-binding regula
3	1497	81.4	359	1	RGHUGY	GTP-binding regula
4	1495	81.3	359	2	S71963	GTP-binding protei
5	1490	81.1	359	1	RGMSQ	GTP-binding regula
6	1489	81.0	359	2	S45700	G-alpha-11 protein
7	1485	80.8	359	2	S45699	GTP-binding regula
8	1483	80.7	353	2	B40891	GTP-binding protei
9	1475	80.3	359	1	RGMS11	GTP-binding regula
10	1472	80.1	353	2	S34347	GTP-binding regula
11	1423.5	77.4	360	2	JN0115	GTP-binding regula
12	1388	75.5	355	2	A40891	GTP-binding protei
13	1388	75.5	355	2	A41534	GTP-binding protei
14	1370.5	74.6	354	2	S33309	GTP-binding regula
15	991	53.9	374	2	B41534	GTP-binding protei
16	965	52.5	374	2	A41096	GTP-binding regula
17	902	49.1	353	2	S71965	GTP-binding regula
18	901	49.0	355	2	I50238	Gi2 protein alpha-
19	896.5	48.8	354	2	S27014	GTP-binding regula
20	895	48.7	355	2	A61031	GTP-binding regula
21	894.5	48.7	354	1	RGHYO2	GTP-binding regula
22	894	48.6	355	1	RGHUI2	GTP-binding regula
23	893.5	48.6	354	1	RGHUO2	GTP-binding regula
24	892	48.5	355	2	S28158	GTP-binding regula
25	891.5	48.5	354	1	RGHUI1	GTP-binding regula
26	891.5	48.5	354	1	RGBOI1	GTP-binding regula
27	891.5	48.5	354	2	T19476	hypothetical prote
28	890.5	48.4	354	1	RGRTI1	GTP-binding regula
29	890	48.4	353	2	T50482	G protein alpha ch
30	887.5	48.3	354	1	RGMSO2	GTP-binding regula
31	887.5	48.3	354	2	A61035	GTP-binding regula
32	886	48.2	355	1	RGRTI2	GTP-binding regula
33	884.5	48.1	354	1	RGFFO2	GTP-binding regula
34	883.5	48.1	354	2	S40509	G-protein - chicke
35	882.5	48.0	354	1	RGRTO2	GTP-binding regula
36	881.5	48.0	354	2	I50237	GTP-binding regula
37	880.5	47.9	354	1	RGXLI1	GTP-binding regula
38	880	47.9	355	1	RGMSI2	GTP-binding regula
39	879.5	47.9	354	2	S28157	GTP-binding regula
40	877.5	47.7	354	2	S40508	GTP-binding regula
41	876.5	47.7	350	1	RGMST1	GTP-binding regula
42	875.5	47.6	354	2	S24362	GTP-binding regula
43	874.5	47.6	354	2	S27013	GTP-binding regula
44	872.5	47.5	354	1	RGFFO1	GTP-binding regula
45	871.5	47.4	350	1	RGBOT1	GTP-binding regula

SUMMARIES

Result No.	Query		Length	DB	ID	Description
	Score	Match				
1	1522	82.8	353	1	GBQ3_DROME	P54400 drosophila
2	1507	82.0	359	1	GB11_MELGA	P45645 meleagris g
3	1497	81.4	353	1	GBQ_RAT	P82471 rattus norv
4	1496	81.4	353	1	GBQ_CANFA	Q28294 canis famil
5	1495	81.3	353	1	GBQ_HUMAN	P50148 homo sapien
6	1493	81.2	359	1	GB11_HUMAN	P29992 homo sapien
7	1490	81.1	353	1	GBQ_MOUSE	P21279 mus musculu
8	1489	81.0	359	1	GB11_XENLA	P43444 xenopus lae
9	1488	81.0	353	1	GBQ_HOMAM	P91950 homarus ame
10	1485	80.8	353	1	GBQ_XENLA	P38410 xenopus lae

11	1483	80.7	359	1	GB11_BOVIN	P38409	bos taurus
12	1475	80.3	359	1	GB11_MOUSE	P21278	mus musculus
13	1472	80.1	353	1	GBQ_LYMST	P38411	lymnaea sta
14	1470	80.0	359	1	GB11_RAT	Q9jid2	rattus norv
15	1452	79.0	353	1	GBQ_PATYE	O15975	patinopecte
16	1437	78.2	353	1	GBQ1_DROME	P23625	drosophila
17	1416	77.0	354	1	GB14_XENLA	O73819	xenopus lae
18	1388	75.5	355	1	GB14_BOVIN	P38408	bos taurus
19	1388	75.5	355	1	GB14_MOUSE	P30677	mus musculus
20	1385	75.4	355	1	GB14_HUMAN	O95837	homo sapien
21	1370.5	74.6	354	1	GBQ_LOLFO	P38412	loligo forb
22	991	53.9	374	1	GB15_MOUSE	P30678	mus musculus
23	990	53.9	374	1	GB15_RAT	O88302	rattus norv
24	965	52.5	374	1	GB15_HUMAN	P30679	homo sapien
25	901	49.0	352	1	GBA1_COACHE	O74227	cochliobolu
26	900	49.0	356	1	GB0_PATYE	O15976	patinopecte
27	897	48.8	352	1	GBA1_EMENI	Q00743	emericella
28	896	48.7	354	1	GBI2_CHICK	P50147	gallus gall
29	891.5	48.5	353	1	GB0_LYMST	P30683	lymnaea sta
30	890.5	48.4	353	1	GB0_HELTI	P51877	helisoma tr
31	890	48.4	352	1	GBA1_CRYPA	Q00580	cryphonectr
32	890	48.4	353	1	GBA1_NEUCR	Q05425	neurospora
33	890	48.4	354	1	GBI2_CANFA	P38400	canis famil
34	889.5	48.4	353	1	GB02_CRILO	P17806	cricketulus
35	889	48.4	354	1	GBI2_HUMAN	P04899	homo sapien
36	888.5	48.3	353	1	GB02_HUMAN	P29777	homo sapien
37	887.5	48.3	354	1	GB0_LOCFI	P38404	locusta mig
38	886.5	48.2	353	1	GBI1_HUMAN	P04898	homo sapien
39	885.5	48.2	353	1	GBI1_RAT	P10824	rattus norv
40	884	48.1	352	1	GBA1_COLTR	O42784	colletotric
41	884	48.1	352	1	GBA1_SPOSC	O74259	sporothrix
42	883	48.0	354	1	GBI2_CAVPO	P38402	cavia porce
43	882.5	48.0	353	1	GB02_MOUSE	P18873	mus musculus
44	881	47.9	352	1	GBA1_MAGGR	O13315	magnaporthe
45	881	47.9	354	1	GBI2_RAT	P04897	rattus norv

SEQ ID NO : 2

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1501	81.7	1276	20	AA49127	phCaR/hmGluR2*Gqi5
2	1501	81.7	1323	20	AA49133	GABA-BR1a*Gqo5 fus
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4	1501	81.7	1397	20	AA49134	pmGluR2/CaR*Galpha
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6	1489	81.0	359	2	S45700	G-alpha-11 protei
7	1485	80.8	359	2	S45699	GTP-binding regula
8	1483	80.7	353	2	B40891	GTP-binding protei
9	1475	80.3	359	1	RGMS11	GTP-binding regula
10	1472	80.1	353	2	S34347	GTP-binding regula
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18	901	49.0	355	2	I50238	Gi2 protein alpha-
19	896.5	48.8	354	2	S27014	GTP-binding regula

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1522	82.8	353	1	GBQ3_DROME	P54400 drosophila
2	1507	82.0	359	1	GB11_MELGA	P45645 meleagris g
3	1497	81.4	353	1	GBQ_RAT	P82471 rattus norv
4	1496	81.4	353	1	GBQ_CANFA	Q28294 canis famil
5	1495	81.3	353	1	GBQ_HUMAN	P50148 homo sapien
6	1493	81.2	359	1	GB11_HUMAN	P29992 homo sapien
7	1490	81.1	353	1	GBQ_MOUSE	P21279 mus musculu
8	1489	81.0	359	1	GB11_XENLA	P43444 xenopus lae
9	1488	81.0	353	1	GBQ_HOMAM	P91950 homarus ame
10	1485	80.8	353	1	GBQ_XENLA	P38410 xenopus lae
11	1483	80.7	359	1	GB11_BOVIN	P38409 bos taurus
12	1475	80.3	359	1	GB11_MOUSE	P21278 mus musculu
13	1472	80.1	353	1	GBQ_LYMST	P38411 lymnaea sta
14	1470	80.0	359	1	GB11_RAT	Q9jid2 rattus norv

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1804	98.2	355	5	Q17386	Q17386 caenorhabdi
2	1496	81.4	359	4	Q9BZB9	Q9bzb9 homo sapien
3	1491	81.1	353	5	Q9U473	Q9u473 panulirus a
4	1472	80.1	353	5	P91955	P91955 limulus pol
5	1426	77.6	353	5	Q9NfZ0	Q9nfz0 calliphora
6	1406	76.5	353	5	Q9NL92	Q9nl92 octopus vul
7	1105.5	60.1	355	5	Q9XZV4	Q9xzv4 geodia cydo
8	1094	59.5	279	5	Q9I7C8	Q9i7c8 drosophila
9	1091.5	59.4	305	5	Q9Y207	Q9y207 hydra magni
10	990	53.9	374	6	Q9TU29	Q9tu29 oryctolagus
11	898	48.9	355	13	O13055	O13055 oryzias lat
12	897	48.8	305	5	Q9Y203	Q9y203 ephydatia f
13	895	48.7	355	13	Q9W6A4	Q9w6a4 squalus aca
14	891.5	48.5	354	5	Q18205	Q18205 caenorhabdi
15	890.5	48.4	354	4	Q9UGA4	Q9uga4 homo sapien
16	888.5	48.3	354	5	Q9NL93	Q9nl93 octopus vul

SEQ ID NO: 3

SUMMARIES

Result	% Query
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No.	Score	Match	Length	DB	ID	Description
1	1806	98.5	355	7	ABR82638	Abr82638 C. elegan
2	1806	98.5	355	7	ABR82630	Abr82630 C. elegan
3	1806	98.5	355	8	ADN22329	Adn22329 Bacterial
4	1766.5	96.3	346	7	ABR82639	Abr82639 C. elegan
5	1525	83.2	353	4	ABB66449	Abb66449 Drosophil
6	1508	82.2	353	5	ABG68585	Abg68585 Mouse G p
7	1508	82.2	359	5	ABG68584	Abg68584 Mouse G p
8	1507	82.2	359	4	AAB99071	Aab99071 Human G-p
9	1507	82.2	359	4	AAB99073	Aab99073 Human G-p
10	1506	82.1	359	5	ABG68610	Abg68610 Human G p
11	1506	82.1	359	7	ADP70780	Adp70780 Minicell
12	1506	82.1	359	8	ADN06136	Adn06136 Human Gq
13	1503	82.0	359	5	ABB09282	Abb09282 G protein
14	1503	82.0	359	7	ADC09617	Adc09617 Human G-p

SUMMARIES

Result	Score	Match	Length	DB	ID	Description
1	1806	98.5	355	2	T15288	hypothetical prote
2	1517	82.7	359	2	S30359	GTP-binding regula
3	1507	82.2	359	1	RGHUGY	GTP-binding regula
4	1501	81.8	359	2	S71963	GTP-binding protei
5	1500	81.8	359	1	RGMSQ	GTP-binding regula
6	1495	81.5	359	2	S45699	GTP-binding regula
7	1493	81.4	353	2	B40891	GTP-binding protei
8	1491	81.3	359	2	S45700	G-alpha-11 protein
9	1485	81.0	359	1	RGMS11	GTP-binding regula
10	1482	80.8	353	2	S34347	GTP-binding regula
11	1419.5	77.4	360	2	JN0115	GTP-binding regula
12	1399	76.3	355	2	A40891	GTP-binding protei
13	1399	76.3	355	2	A41534	GTP-binding protei
14	1380.5	75.3	354	2	S33309	GTP-binding regula
15	996	54.3	374	2	B41534	GTP-binding protei

SUMMARIES

Result	Score	Match	Length	DB	ID	Description
1	1806	98.5	355	2	Q17386	Q17386 caenorhabdi
2	1547	84.4	303	2	Q8T3G5	Q8t3g5 caenorhabdi
3	1528	83.3	353	2	Q76FN3	Q76fn3 bombyx mori
4	1523	83.0	353	2	Q6QM13	Q6qm13 lytechinus
5	1517	82.7	359	1	GB11_MELGA	P45645 meleagris g
6	1517	82.7	359	2	Q71RI7	Q71ri7 gallus gall
7	1516	82.7	353	2	Q6QM11	Q6qm11 strongyloce
8	1516	82.7	353	2	Q7PHK1	Q7phk1 anopheles g
9	1514	82.6	353	2	Q6ITD0	Q6itd0 penaeus van
10	1507	82.2	353	1	GBQ_RAT	P82471 rattus norv
11	1506	82.1	353	1	GBQ_CANFA	Q28294 canis famil
12	1506	82.1	353	1	GBQ_HUMAN	P50148 homo sapien
13	1506	82.1	359	2	Q6NT27	Q6nt27 homo sapien
14	1504	82.0	359	2	Q6P7M2	Q6p7m2 xenopus tro
15	1503	82.0	359	1	GB11_HUMAN	P29992 homo sapien
16	1501	81.8	353	2	Q9U473	Q9u473 panulirus a
17	1500	81.8	353	1	GBQ_MOUSE	P21279 mus musculu
18	1498	81.7	353	1	GBQ_HOMAM	P91950 homarus

SEQ ID NO : 4

SUMMARIES

Result	Query
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No.	Score	Match	Length	DB	ID	Description
1	1761	95.6	355	7	ABR82638	Abr82638 C. elegan
2	1761	95.6	355	7	ABR82630	Abr82630 C. elegan
3	1761	95.6	355	8	ADN22329	Adn22329 Bacterial
4	1727	93.8	346	7	ABR82639	Abr82639 C. elegan
5	1480	80.3	353	4	ABB66449	Abb66449 Drosophil
6	1463	79.4	353	5	ABG68585	Abg68585 Mouse G p
7	1463	79.4	359	5	ABG68584	Abg68584 Mouse G p
8	1462	79.4	359	4	AAB99071	Aab99071 Human G-p
9	1462	79.4	359	4	AAB99073	Aab99073 Human G-p
10	1461	79.3	359	5	ABG68610	Abg68610 Human G p
11	1461	79.3	359	7	ADP70780	Adp70780 Minicell
12	1461	79.3	359	8	ADN06136	Adn06136 Human Gq
13	1458	79.2	359	5	ABB09282	Abb09282 G protein
14	1458	79.2	359	7	ADC09617	Adc09617 Human G-p
15	1456	79.0	353	4	AAB99072	Aab99072 Human G-p
16	1456	79.0	353	5	ABG68599	Abg68599 Human G p
17	1456	79.0	353	5	ABB09281	Abb09281 G protein
18	1456	79.0	353	7	ABR82631	Abr82631 C. elegan
19	1456	79.0	353	7	ADC09616	Adc09616 Human G-p

SUMMARIES

Result		Query				Description
No.	Score	Match	Length	DB	ID	
1	1761	95.6	355	2	T15288	hypothetical prote
2	1472	79.9	359	2	S30359	GTP-binding regula
3	1462	79.4	359	1	RGHUGY	GTP-binding regula
4	1456	79.0	359	2	S71963	GTP-binding protei
5	1455	79.0	359	1	RGMSQ	GTP-binding regula
6	1450	78.7	359	2	S45699	GTP-binding regula
7	1448	78.6	353	2	B40891	GTP-binding protei
8	1446	78.5	359	2	S45700	G-alpha-11 protein
9	1440	78.2	359	1	RGMS11	GTP-binding regula
10	1437	78.0	353	2	S34347	GTP-binding regula
11	1388.5	75.4	360	2	JN0115	GTP-binding regula
12	1354	73.5	355	2	A40891	GTP-binding protei
13	1354	73.5	355	2	A41534	GTP-binding protei
14	1335.5	72.5	354	2	S33309	GTP-binding regula
15	995	54.0	374	2	B41534	GTP-binding protei

SUMMARIES

Result		Query						
No.	Score	Match	Length	DB	ID	Description		
1	1761	95.6	355	2	Q17386	Q17386	caenorhabdi	
2	1502	81.5	303	2	Q8T3G5	Q8t3g5	caenorhabdi	
3	1483	80.5	353	2	Q76FN3	Q76fn3	bombyx mori	
4	1478	80.2	353	2	Q6QM13	Q6qml3	lytechinus	
5	1472	79.9	359	1	GB11_MELGA	P45645	meleagris g	
6	1472	79.9	359	2	Q71RI7	Q71ri7	gallus gall	
7	1471	79.9	353	2	Q6QM11	Q6qml1	strongyloce	
8	1471	79.9	353	2	Q7PHK1	Q7phk1	anopheles g	
9	1469	79.8	353	2	Q6ITD0	Q6itd0	penaeus van	
10	1462	79.4	353	1	GBQ_RAT	P82471	rattus norv	
11	1461	79.3	353	1	GBQ_CANFA	Q28294	canis famil	
12	1461	79.3	353	1	GBQ_HUMAN	P50148	homo sapien	
13	1461	79.3	359	2	Q6NT27	Q6nt27	homo sapien	
14	1459	79.2	359	2	Q6P7M2	Q6p7m2	xenopus tro	
15	1458	79.2	359	1	GB11_HUMAN	P29992	homo sapien	

SEQ ID NO: 5

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1817	98.7	355	7	ABR82638	Abr82638 C. elegan
2	1817	98.7	355	7	ABR82630	Abr82630 C. elegan
3	1817	98.7	355	8	ADN22329	Adn22329 Bacterial
4	1774.5	96.4	346	7	ABR82639	Abr82639 C. elegan
5	1526	82.9	353	4	ABB66449	Abb66449 Drosophil
6	1519	82.5	1276	2	AAy49127	Aay49127 phCaR/hmG
7	1519	82.5	1276	5	AAO15093	Aao15093 Human pHc
8	1519	82.5	1323	2	AAy49133	Aay49133 GABA-BR1a
9	1519	82.5	1323	5	AAO15099	Aao15099 Human GAB
10	1519	82.5	1394	2	AAy49129	Aay49129 pmGluR2/C
11	1519	82.5	1394	5	AAO15095	Aao15095 Human pmG
12	1519	82.5	1397	2	AAy49134	Aay49134 pmGluR2/C
13	1519	82.5	1397	5	AAO15100	Aao15100 Human pmG
14	1519	82.5	1402	5	AAO15105	Aao15105 Human pH2
15	1519	82.5	1418	2	AAy49131	Aay49131 mGluR8/Ca
16	1519	82.5	1418	5	AAO15097	Aao15097 Human mGl
17	1519	82.5	1421	5	AAO15103	Aao15103 Human phm
18	1519	82.5	1422	5	AAO15102	Aao15102 Human phm

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1817	98.7	355	2	T15288	hypothetical prote
2	1513	82.2	359	2	S30359	GTP-binding regula
3	1503	81.6	359	1	RGHUGY	GTP-binding regula
4	1502	81.6	359	2	S45700	G-alpha-11 protein
5	1500	81.5	359	2	S71963	GTP-binding protei
6	1496	81.3	359	1	RGMSQ	GTP-binding regula
7	1491	81.0	359	2	S45699	GTP-binding regula
8	1489	80.9	353	2	B40891	GTP-binding protei
9	1481	80.4	359	1	RGMS11	GTP-binding regula
10	1478	80.3	353	2	S34347	GTP-binding regula
11	1423.5	77.3	360	2	JN0115	GTP-binding regula
12	1393	75.7	355	2	A40891	GTP-binding protei
13	1393	75.7	355	2	A41534	GTP-binding protei
14	1376.5	74.8	354	2	S33309	GTP-binding regula
15	993	53.9	374	2	B41534	GTP-binding protei
16	967	52.5	374	2	A41096	GTP-binding regula

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1817	98.7	355	2	Q17386	Q17386 caenorhabdi
2	1558	84.6	303	2	Q8T3G5	Q8t3g5 caenorhabdi
3	1529	83.1	353	2	Q76FN3	Q76fn3 bombyx mori
4	1519	82.5	353	2	Q6QM13	Q6qml3 lytechinus
5	1517	82.4	353	2	Q7PHK1	Q7phk1 anopheles g
6	1515	82.3	359	2	Q6P7M2	Q6p7m2 xenopus tro
7	1513	82.2	359	1	GB11_MELGA	P45645 meleagris g
8	1513	82.2	359	2	Q71RI7	Q71ri7 gallus gall
9	1512	82.1	353	2	Q6QM11	Q6qml1 strongyloce
10	1510	82.0	353	2	Q6ITD0	Q6itd0 penaeus van
11	1503	81.6	353	1	GBQ_RAT	P82471 rattus norv
12	1503	81.6	359	2	Q8AVH0	Q8avh0 xenopus lae
13	1502	81.6	353	1	GBQ_CANFA	Q28294 canis famil
14	1502	81.6	353	1	GBQ_HUMAN	P50148 homo sapien
15	1502	81.6	359	1	GB11_XENLA	P43444 xenopus lae

16	1502	81.6	359	2	Q6NT27	Q6nt27 homo sapien
17	1499	81.4	359	1	GB11_HUMAN	P29992 homo sapien
18	1497	81.3	353	2	Q9U473	Q9u473 panulirus a

SEQ ID NO : 41

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1800	98.4	353	4	ABB66449	Abb66449 Drosophil
2	1555	85.0	1276	2	AA49127	Aay49127 phCaR/hmG
3	1555	85.0	1276	5	AA015093	Aao15093 Human phC
4	1555	85.0	1323	2	AA49133	Aay49133 GABA-BR1a
5	1555	85.0	1323	5	AA015099	Aao15099 Human GAB
6	1555	85.0	1394	2	AA49129	Aay49129 pmGluR2/C
7	1555	85.0	1394	5	AA015095	Aao15095 Human pmG
8	1555	85.0	1397	2	AA49134	Aay49134 pmGluR2/C
9	1555	85.0	1397	5	AA015100	Aao15100 Human pmG
10	1555	85.0	1402	5	AA015105	Aao15105 Human ph2
11	1555	85.0	1418	2	AA49131	Aay49131 mGluR8/Ca
12	1555	85.0	1418	5	AA015097	Aao15097 Human mGl
13	1555	85.0	1421	5	AA015103	Aao15103 Human phm
14	1555	85.0	1422	5	AA015102	Aao15102 Human phm

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1615.5	88.3	360	2	JN0115	GTP-binding regula
2	1549	84.7	359	2	S71963	GTP-binding protei
3	1539	84.1	359	1	RGMSQ	GTP-binding regula
4	1538	84.1	359	2	S45700	G-alpha-11 protein
5	1533	83.8	359	2	S30359	GTP-binding regula
6	1521	83.2	359	2	S45699	GTP-binding regula
7	1520	83.1	355	2	T15288	hypothetical prote
8	1510	82.6	353	2	B40891	GTP-binding protei
9	1509	82.5	359	1	RGMS11	GTP-binding regula
10	1507	82.4	359	1	RGHUGY	GTP-binding regula
11	1489	81.4	353	2	S34347	GTP-binding regula
12	1417	77.5	355	2	A40891	GTP-binding protei
13	1401.5	76.6	354	2	S33309	GTP-binding regula
14	1393	76.2	355	2	A41534	GTP-binding protei
15	1033	56.5	374	2	B41534	GTP-binding protei
16	1017	55.6	374	2	A41096	GTP-binding regula

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1646	90.0	353	2	Q7PHK1	Q7phk1 anopheles g
2	1631	89.2	353	2	Q76FN3	Q76fn3 bombyx mori
3	1629	89.1	353	1	GBQ_DROME	P23625 drosophila
4	1602	87.6	353	2	Q8T6P8	Q8t6p8 mamestra br
5	1599	87.4	353	2	Q6ITD0	Q6itd0 penaeus van
6	1599	87.4	353	2	Q9U473	Q9u473 panulirus a
7	1598	87.4	353	1	GBQ_HOMAM	P91950 homarus ame
8	1571	85.9	353	2	Q9NFZ0	Q9nfh0 calliphora
9	1568	85.7	353	2	P91955	P91955 limulus pol
10	1550	84.7	353	1	GBQ_CANFA	Q28294 canis famil
11	1550	84.7	353	1	GBQ_HUMAN	P50148 homo sapien
12	1550	84.7	359	2	Q6NT27	Q6nt27 homo sapien
13	1548	84.6	359	2	Q6P7M2	Q6p7m2 xenopus tro
14	1546	84.5	353	1	GBQ_RAT	P82471 rattus norv
15	1539	84.1	353	1	GBQ_MOUSE	P21279 mus musculu

16	1539	84.1	359	2	Q8AVH0
17	1538	84.1	359	1	GB11_XENLA

Q8avh0	xenopus	lae
P43444	xenopus	lae